SEQUENCE LISTING

<110> Colucci, M. Gabriella
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<120> Progenitor Cell Preservation Factors and Methods for and Products of Their Use

<130> 108236.119

<140> US 09/476,485
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<151> 1997-06-24

<160> 57

<170> PatentIn version 3.0

<210> 1
<211> 939
<212> DNA
<213> Artificial Sequence

B1

<220>
<223> D1-FRIL.

<400> 1
gcacagtcat tgtcatttag tttcaccaag tttgatccta accaagagga tcttatcttc 60

caaggtcatg ccacttctac aaacaatgtc ttacaagtca ccaagttaga cagtgcagga 120

aaccctgtga gttctagtgc gggaagagtg ttatattctg caccattgcg cctttgggaa 180

gactctgcgg tattgacaag ctttgacacc attatcaact ttgaaatctc aacaccttac 240

acttctcgta tagctgatgg cttggccttc ttcattgcac cacctgactc tgtcatcagt 300

tatcatggtg gttttcttgg actctttccc aacgcaaaca ctctcaacaa ctcttccacc 360

tctgaaaacc aaaccaccac taaggctgca tcaagcaacg ttgttgctgt tgaatttgac 420

acctatctta atcccgatta tggtgatcca aactacatac acatcggaat tgacgtcaac 480

tctattagat ccaaggtaac tgctaagtgg gactggcaaa atgggaaaat agccactgca 540

cacattagct ataactctgt ctctaaaaga ctatctgtta ctagttatta tgctgggagt 600

aaacctgcga ctctctccta tgatattgag ttacatacag tgcttcctga atgggtcaga 660

gtagggttat ctgcttcaac tggacaagat aaagaaagaa ataccgttca ctcatggtct 720

ttcacttcaa gcttgtggac caatgtggcg aagaaggaga atgaaaacaa gtatattaca 780

agaggcgttc tgtgatgata tatgtgtatc aatgattttc tatgttataa gcatgtaatg 840

tgcgatgagt caataatcac aagtacagtg tagtacttgt atgttgtttg tgtaagagtc 900

agtttgcttt taataataac aagtgcagtt agtacttgt 939

<210> 2
<211> 264
<212> PRT
<213> Artificial Sequence

<220>
<223> D1-FRIL.

<400> 2

Ala Gly Ser Leu Ser Phe Ser Phe Thr Lys Phe Asp Pro Asn Gln Glu
1 5 10 15

Asp Leu Ile Phe Gln Gly His Ala Thr Ser Thr Asn Asn Val Leu Gln
20 25 30

Val Thr Lys Leu Asp Ser Ala Gly Asn Pro Val Ser Ser Ser Ala Gly
35 40 45

Arg Val Leu Tyr Ser Ala Pro Leu Arg Leu Trp Glu Asp Ser Ala Val
50 55 60

Leu Thr Ser Phe Asp Thr Ile Ile Asn Phe Glu Ile Ser Thr Pro Tyr
65 70 75 80

Thr Ser Arg Ile Ala Asp Gly Leu Ala Phe Phe Ile Ala Pro Pro Asp
85 90 95

Ser Val Ile Ser Tyr His Gly Gly Phe Leu Gly Leu Phe Pro Asn Ala
100 105 110

Asn Thr Leu Asn Asn Ser Ser Thr Ser Glu Asn Gln Thr Thr Thr Lys
115 120 125

Ala Ala Ser Ser Asn Val Val Ala Val Glu Phe Asp Thr Tyr Leu Asn
130 135 140

Pro Asp Tyr Gly Asp Pro Asn Tyr Ile His Ile Gly Ile Asp Val Asn
145 150 155 160

Ser Ile Arg Ser Lys Val Thr Ala Lys Trp Asp Trp Gln Asn Gly Lys
165 170 175

Ile Ala Thr Ala His Ile Ser Tyr Asn Ser Val Ser Lys Arg Leu Ser
180 185 190

Val Thr Ser Tyr Tyr Ala Gly Ser Lys Pro Ala Thr Leu Ser Tyr Asp
195 200 205

Ile Glu Leu His Thr Val Leu Pro Glu Trp Val Arg Val Gly Leu Ser
210 215 220

Ala Ser Thr Gly Gln Asp Lys Glu Arg Asn Thr Val His Ser Trp Ser
225 230 235 240

Phe Thr Ser Ser Leu Trp Thr Asn Val Ala Lys Lys Glu Asn Glu Asn
245 250 255

Lys Tyr Ile Thr Arg Gly Val Leu
260

<210> 3
<211> 1005
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of the naturally-occurring D1-FRIL protein.

<400> 3
atggcttcct ccaacttact caccctagcc ctcttccttg tgcttctcac ccacgcaaac 60

tcagccgcac agtcattgtc atttagtttc accaagtttg atcctaacca agaggatctt 120

atcttccaag gtcatgccac ttctacaaac aatgtcttac aagtcaccaa gttagacagt 180

gcaggaaacc ctgtgagttc tagtgcggga agagtgttat attctgcacc attgcgcctt 240

tgggaagact ctgcggtatt gacaagcttt gacaccatta tcaactttga aatctcaaca 300

ccttacactt ctcgtatagc tgatggcttg gccttcttca ttgcaccacc tgactctgtc 360

atcagttatc atggtggttt tcttggactc tttcccaacg caaacactct caacaactct 420

tccacctctg aaaaccaaac caccactaag gctgcatcaa gcaacgttgt tgctgttgaa 480

tttgacacct atcttaatcc cgattatggt gatccaaact acatacacat cggaattgac 540

gtcaactcta ttagatccaa ggtaactgct aagtgggact ggcaaaatgg gaaaatagcc 600

actgcacaca ttagctataa ctctgtctct aaaagactat ctgttactag ttattatgct 660

gggagtaaac ctgcgactct ctcctatgat attgagttac atacagtgct tcctgaatgg 720

gtcagagtag ggttatctgc ttcaactgga caagataaag aaagaaatac cgttcactca 780

tggtctttca cttcaagctt gtggaccaat gtggcgaaga aggagaatga aaacaagtat 840

attacaagag gcgttctgtg atgatatatg tgtatcaatg attttctatg ttataagcat 900

gtaatgtgcg atgagtcaat aatcacaagt acagtgtagt acttgtatgt tgtttgtgta 960

agagtcagtt tgcttttaat aataacaagt gcagttagta cttgt 1005

<210> 4
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal sequence from the FRIL family isolated from Dolichos lab lab

<400> 4

Met Ala Ser Ser Asn Leu Leu Thr Leu Ala Leu Phe Leu Val Leu Leu
1 5 10 15

Thr His Ala Asn Ser Ala
20

<210> 5
<211> 914
<212> DNA
<213> Artificial Sequence

<220>
<223> Pv-FRIL.

<400> 5
gctcagtcat tatcttttaa ctttaccaag tttgatcttg accaaaaaga tcttatcttc 60

caaggtgatg ccacttctac aaacaatgtc ttacaactca ctaagttaga cagtggagga 120

aaccctgtgg gtgctagtgt gggaagagtg ttattctctg caccatttca tctttgggaa 180

aactctatgg cagtgtcaag ctttgaaact aatctcacca ttcaaatctc aacacctcac 240

ccttattatg cagctgatgg ctttgccttc ttccttgcac cacatgacac tgtcatccct 300

ccaaattctt ggggcaaatt ccttggactc tactcaaacg ttttcagaaa ctccccccacc 360

tctgaaaacc aaagctttgg tgatgtcaat actgactcaa gagttgttgc tgtcgaattt 420

gacaccttcc ctaatgccaa tattgatcca aattacagac acattggaat cgatgtgaac 480

tctattaagt ccaaggaaac tgctaggtgg gagtggcaaa atgggaaaac ggccactgca 540

cgcatcagct ataactctgc ctctaaaaaa tcaactgtta ctacgtttta tcctgggatg 600

gaagttgtgg ctctctccca tgatgttgac ttacatgcag agcttcctga atgggttaga 660

gtagggttat ctgcttcaac tggagaggag aaacaaaaaa ataccattat ctcatggtct 720

ttcacttcaa gcttgaagaa caacgaggtg aaggagccga aagaagacat gtatattgca 780

aacgttgtgc gatcatatac atggatcaat gacgttctat cttatataag caataaataa 840

atgtatgatg cactcaataa taatcacaag tacgtacggt gtagtacttg tatgttgttt 900

atgaaaaaaa aaaa 914

<210> 6
<211> 303
<212> PRT
<213> Artificial Sequence

<220>
<223> Pv-FRIL.

<400> 6

Ala Gln Ser Leu Ser Phe Asn Phe Thr Lys Phe Asp Leu Asp Gln Lys
1 5 10 15

Asp Leu Ile Phe Gln Gly Asp Ala Thr Ser Thr Asn Asn Val Leu Gln
20 25 30

Leu Thr Lys Leu Asp Ser Gly Gly Asn Pro Val Gly Ala Ser Val Gly
35 40 45

Arg Val Leu Phe Ser Ala Pro Phe His Leu Trp Glu Asn Ser Met Ala
50 55 60

Val Ser Ser Phe Glu Thr Asn Leu Thr Ile Gln Ile Ser Thr Pro His
65 70 75 80

Pro Tyr Tyr Ala Ala Asp Gly Phe Ala Phe Phe Leu Ala Pro His Asp
85 90 95

Thr Val Ile Pro Pro Asn Ser Trp Gly Lys Phe Leu Gly Leu Tyr Ser
100 105 110

Asn Val Phe Arg Asn Ser Pro Thr Ser Glu Asn Gln Ser Phe Gly Asp
115 120 125

Val Asn Thr Asp Ser Arg Val Val Ala Val Glu Phe Asp Thr Phe Pro
130 135 140

Asn Ala Asn Ile Asp Pro Asn Tyr Arg His Ile Gly Ile Asp Val Asn
145 150 155 160

Ser Ile Lys Ser Lys Glu Thr Ala Arg Trp Glu Trp Gln Asn Gly Lys
165 170 175

Thr Ala Thr Ala Arg Ile Ser Tyr Asn Ser Ala Ser Lys Lys Ser Thr
180 185 190

Val Thr Thr Phe Tyr Pro Gly Met Glu Val Val Ala Leu Ser His Asp
195 200 205

Val Asp Leu His Ala Glu Leu Pro Glu Trp Val Arg Val Gly Leu Ser
210 215 220

Ala Ser Thr Gly Glu Glu Lys Gln Lys Asn Thr Ile Ile Ser Trp Ser

225 230 235 240

Phe Thr Ser Ser Leu Lys Asn Asn Glu Val Lys Glu Pro Lys Glu Asp
245 250 255

Met Tyr Ile Ala Asn Val Val Arg Ser Tyr Thr Trp Ile Asn Asp Val
260 265 270

Leu Ser Tyr Ile Ser Asn Lys Met Tyr Asp Ala Leu Asn Asn Asn His
275 280 285

Lys Tyr Val Arg Cys Ser Thr Cys Met Leu Phe Met Lys Lys Lys
290 295 300

<210> 7
<211> 678
<212> DNA
<213> Artificial Sequence

<220>
<223> YamFril partial mRNA sequence.

<400> 7
acgaagttcg acagcgacca aaaggatctt atgttccaag gtcataccat ttctagcagc 60

aatgtcatac aactcaccaa gttagacagt aatggaaacc ctgtgagtac cagtgtggga 120

agagtgttat actctgcacc attgcgcctt tgggaaagct ctacagtagt gtcaaccttt 180

gagaccactt tcacctttca aatctcaaca ccttacacta gtcctcctgg tgatgggctc 240

gccttcttcc ttgcaccata tgacactgtc atccctccaa attctgctgg caatcttctt 300

ggactctttc ctaacttaaa tgctttaaga aactccacca ccagtaaaga aaccactatt 360

gatgtcaatg ctgcatctaa caacgttgtt gccgttgaat ttgacaccta ccctaacgac 420

aatattggtg atccaagata caaacacatt ggaatcgatg tcaactctat caggtccaag 480

gcaactgttg cgtgggactg gcaaaatggg aaaacagcca ctgcacacat cagctataac 540

tctgcctcta aaagactatc tgttactact ttttatcctg ggggtaaagc tgtgagtctt 600

tcccatgacg ttgagctcac tcaagtgctt cctcaatgga ttagagtagg gttctctgct 660

tcaacaggat tagagaaa 678

<210> 8
<211> 234
<212> PRT
<213> Artificial Sequence

<220>
<223> YamFril deduced amino acid squence.

<400> 8

Ala Gln Ser Val Ser Phe Thr Phe Thr Lys Phe Asp Ser Asp Gln Lys
1 5 10 15

Asp Leu Met Phe Gln Gly His Thr Ile Ser Ser Ser Asn Val Ile Gln
20 25 30

Leu Thr Lys Leu Asp Ser Asn Gly Asn Pro Val Ser Thr Ser Val Gly
35 40 45

Arg Val Leu Tyr Ser Ala Pro Leu Arg Leu Trp Glu Ser Ser Thr Val
50 55 60

Val Ser Thr Phe Glu Thr Thr Phe Thr Phe Gln Ile Ser Thr Pro Tyr
65 70 75 80

Thr Ser Pro Pro Gly Asp Gly Leu Ala Phe Phe Leu Ala Pro Tyr Asp
85 90 95

Thr Val Ile Pro Pro Asn Ser Ala Gly Asn Leu Leu Gly Leu Phe Pro
100 105 110

Asn Leu Asn Ala Leu Arg Asn Ser Thr Thr Ser Lys Glu Thr Thr Ile
115 120 125

Asp Val Asn Ala Ala Ser Asn Asn Val Val Ala Val Glu Phe Asp Thr
130 135 140

Tyr Pro Asn Asp Asn Ile Gly Asp Pro Tyr Arg Lys His Ile Gly Ile
145 150 155 160

Asp Val Asn Ser Ile Arg Ser Lys Ala Thr Val Ala Trp Asp Trp Gln
165 170 175

Asn Gly Lys Thr Ala Thr Ala His Ile Ser Tyr Asn Ser Ala Ser Lys
180 185 190

Arg Leu Ser Val Thr Thr Phe Tyr Pro Gly Gly Lys Ala Val Ser Leu
195 200 205

Ser His Asp Val Glu Leu Thr Gln Val Leu Pro Gln Trp Ile Arg Val
210 215 220

Gly Phe Ser Ala Ser Thr Gly Leu Glu Lys
225 230

<210> 9
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Beta band polypeptide.

<400> 9

Ala Gln Ser Val Ser Phe Thr Phe Thr Lys Phe Asp Ser Asp Gln
1 5 10 15

<210> 10
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Alpha band polypeptide.

<220>
<221> PEPTIDE
<222> (14)..(14)
<223> Amino acid 14 is Xaa wherein Xaa = any amino acid.

<400> 10

Ala Ala Ser Asn Asn Val Val Ala Val Glu Phe Asp Thr Xaa Pro Asn
1 5 10 15

<210> 11
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> MLA degenerate oligonucleotide primer.

<220>
<221> misc_feature
<222> (3)..(21)
<223> Nucleotides 3, 18 and 21 are n wherein n = a or g.

<220>
<221> misc_feature
<222> (6)..(15)
<223> Nucleotides 6, 9, and 15 are n wherein n = t or c.

<220>
<221> misc_feature
<222> (12)..(12)
<223> Nucleotide 12 is n wherein n = a or t.

<400> 11
aanttnganc cnaancanga nga 23

<210> 12

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> MLZ degenerate oligonucleotide primer.

<220>
<221> misc_feature
<222> (3)..(3)
<223> Nucleotide 3 is n wherein n = a or t.

<220>
<221> misc_feature
<222> (6)..(15)
<223> Nucleotides 6 and 15 are n wherein n = a or g.

<220>
<221> misc_feature
<222> (9)..(9)
<223> Nucleotide 9 is n wherein n = t or c.

<400> 12
ttnccnttnt gccantccca 20

<210> 13
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> primer.

<400> 13
gtaccgagct cggat 15

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> primer.

<400> 14
tctagatgca tgctcgag 18

<210> 15
<211> 22
<212> DNA

<213> Artificial Sequence

<220>
<223> MLX primer.

<400> 15
gttggacgtc aattccgatg tg 22

<210> 16
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> MLI degenerate primer.

<220>
<221> misc_feature
<222> (3)..(15)
<223> Nucleotides 3, 9, 12 and 15 are n wherein n = t or c.

<220>
<221> misc_feature
<222> (6)..(6)
<223> Nucleotide 6 is n wherein n = a or g.

<400> 16
gcncantcnc tntcntt 17

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligo(dT) anchor primer.

<400> 17
gaccacgcgt atcgatgtcg ac 22

<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> MLB primer.

<400> 18

aagttagaca gtgcaggaaa c 21

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> MLII primer.

<400> 19
gcacagtcat tgtcatttag 20

<210> 20
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> D1-FRIL.

<400> 20

Tyr Leu Asn Pro Asp Tyr Gly Asp Pro Asn Tyr Ile His Ile Gly Ile
1 5 10 15

Asp Val

<210> 21
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Pea.

<400> 21

Phe Tyr Asn Ala Ala Trp Asp Pro Ser Asn Arg Asp Arg His Ile Gly
1 5 10 15

Ile Asp Val

<210> 22
<211> 1005
<212> DNA
<213> Artificial Sequence

<220>
<223> SpDLA.

<400> 22
atggcttcct ccaacttact caccctagcc ctcttccttg tgcttctcac ccacgcaaac 60

tcagccgcac agtcattgtc atttagtttc accaagtttg atcctaacca agaggatctt 120

atcttccaag gtcatgccac ttctacaaac aatgtcttac aagtcaccaa gttagacagt 180

gcaggaaacc ctgtgagttc tagtgcggga agagtgttat attctgcacc attgcgcctt 240

tgggaagact ctgcggtatt gacaagcttt gacaccatta tcaactttga aatctcaaca 300

ccttacactt ctcgtatagc tgatggcttg gccttcttca ttgcaccacc tgactctgtc 360

atcagttatc atggtggttt tcttggactc tttcccaacg caaacactct caacaactct 420

tccacctctg aaaaccaaac caccactaag gctgcatcaa gcaacgttgt tgctgttgaa 480

tttgacacct atcttaatcc cgattatggt gatccaaact acatacacat cggaattgac 540

gtcaactcta ttagatccaa ggtaactgct aagtgggact ggcaaaatgg gaaaatagcc 600

actgcacaca ttagctataa ctctgtctct aaaagactat ctgttactag ttattatgct 660

gggagtaaac ctgcgactct ctcctatgat attgagttac atacagtgct tcctgaatgg 720

gtcagagtag ggttatctgc ttcaactgga caagataaag aaagaaatac cgttcactca 780

tggtctttca cttcaagctt gtggaccaat gtggcgaaga aggagaatga aaacaagtat 840

attacaagag gcgttctgtg atgatatatg tgtatcaatg attttctatg ttataagcat 900

gtaatgtgcg atgagtcaat aatcacaagt acagtgtagt acttgtatgt tgtttgtgta 960

agagtcagtt tgcttttaat aataacaagt gcagttagta cttgt 1005

<210> 23
<211> 286
<212> PRT
<213> Artificial Sequence

<220>
<223> SpDLA.

<400> 23

Met Ala Ser Ser Asn Leu Leu Thr Leu Ala Leu Phe Leu Val Leu Leu
1 5 10 15

Thr His Ala Asn Ser Ala Ala Gln Ser Leu Ser Phe Ser Phe Thr Lys
20 25 30

Phe Asp Pro Asn Gln Glu Asp Leu Ile Phe Gln Gly His Ala Thr Ser
35 40 45

Thr Asn Asn Val Leu Gln Val Thr Lys Leu Asp Ser Ala Gly Asn Pro
50 55 60

Val Ser Ser Ser Ala Gly Arg Val Leu Tyr Ser Ala Pro Leu Arg Leu
65 70 75 80

Trp Glu Asp Ser Ala Val Leu Thr Ser Phe Asp Thr Ile Ile Asn Phe
85 90 95

Glu Ile Ser Thr Pro Tyr Thr Ser Arg Ile Ala Asp Gly Leu Ala Phe
100 105 110

Phe Ile Ala Pro Pro Asp Ser Val Ile Ser Tyr His Gly Gly Phe Leu
115 120 125

Gly Leu Phe Pro Asn Ala Asn Thr Leu Asn Asn Ser Ser Thr Ser Glu
130 135 140

Asn Gln Thr Thr Thr Lys Ala Ala Ser Ser Asn Val Val Ala Val Glu
145 150 155 160

Phe Asp Thr Tyr Leu Asn Pro Asp Tyr Gly Asp Pro Asn Tyr Ile His
165 170 175

Ile Gly Ile Asp Val Asn Ser Ile Arg Ser Lys Val Thr Ala Lys Trp
180 185 190

Asp Trp Gln Asn Gly Lys Ile Ala Thr Ala His Ile Ser Tyr Asn Ser
195 200 205

Val Ser Lys Arg Leu Ser Val Thr Ser Tyr Tyr Ala Gly Ser Lys Pro
210 215 220

Ala Thr Leu Ser Tyr Asp Ile Glu Leu His Thr Val Leu Pro Glu Trp
225 230 235 240

Val Arg Val Gly Leu Ser Ala Ser Thr Gly Gln Asp Lys Glu Arg Asn
245 250 255

Thr Val His Ser Trp Ser Phe Thr Ser Ser Leu Trp Thr Asn Val Ala
260 265 270

Lys Lys Glu Asn Glu Asn Lys Tyr Ile Thr Arg Gly Val Leu
275 280 285

<210> 24
<211> 8
<212> PRT
<213> Dolichos lablab

<220>
<221> PEPTIDE
<222> (7)..(7)
<223> Amino acid 7 is Xaa wherein Xaa = any amino acid.

<400> 24

Thr Asn Asn Val Leu Gln Xaa Thr
1 5

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> MutI primer.

<400> 25
ccataatcgg gatcaagata ggtg 24

<210> 26
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> MutII primer.

<400> 26
cacctatctt gatcccgatt atgg 24

<210> 27
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> M1 Forw primer.

<400> 27
aactcagccg cacagtcatt gtca 24

<210> 28
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> APEcoRI primer.

<400> 28

gaattcgacc acgcgtatcg atgtcgac 28

<210> 29
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Sigforw primer.

<400> 29
gaattcatgg cttcctccaa c 21

<210> 30
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Sigrev primer.

<400> 30
tgactgtgcg gctgagtttg cgtgggtg 28

<210> 31
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide corresponding to Pv-FRIL.

<220>
<221> PEPTIDE
<222> (7)..(7)
<223> Amino acid 7 is Xaa wherein Xaa = Asn, Cys or Ser.

<400> 31

Ala Gln Ser Leu Ser Phe Xaa Phe Thr Lys Phe Asp Leu Asp
1 5 10

<210> 32
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Polypeptide of 18 kDa.

<220>
<221> PEPTIDE
<222> (7)..(7)
<223> Amino acid 7 is Xaa wherein Xaa = unknown amino acid.

<400> 32

Ala Gln Ser Leu Ser Phe Xaa Phe Thr Lys Asp Ala Leu Asp
1 5 10

<210> 33
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Aminoterminal sequence.

<220>
<221> PEPTIDE
<222> (12)..(12)
<223> Amino acid 12 is Xaa wherein Xaa = unknown amino acid.

<400> 33

Thr Asp Ser Arg Val Val Ala Val Glu Phe Asp Xaa Phe Pro
1 5 10

<210> 34
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Aminoterminal polypeptide.

<220>
<221> PEPTIDE
<222> (7)..(7)
<223> Amino acid 7 is Xaa wherein Xaa = unknown amino acid.

<400> 34

Ala Gln Ser Leu Ser Phe Xaa Phe Lys Phe Asp Pro Asn
1 5 10

<210> 35
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Aminoterminal polypeptide.

<400> 35

Thr Asp Ser Arg Val Val Ala Val Glu Asp Phe
1 5 10

<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Degenerate oligonucleotide PVBeta1.

<220>
<221> misc_feature
<222> (18)..(18)
<223> Nucleotide 18 is n wherein n = any nucleotide.

<400> 36
ttyacyaart tygayytnga 20

<210> 37
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Degenerate oligonucleotide PVBeta2.

<400> 37
atyttycarg gwgaygc 17

<210> 38
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Degenerate oligonucleotide PVAlfa1.

<400> 38
ttracrtcra twccratrtg 20

<210> 39

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Degenerate oligonucleotide PVA1fa2.

<400> 39
tarttwggrt cratrttrgc rtt 23

<210> 40
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> PV3 PCR-Anchor primer.

<400> 40
caatgtctta caactcacta ag 22

<210> 41
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> PV4 PCR-Anchor primer.

<400> 41
agtgtgggaa gagtgttatt c 21

<210> 42
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> SPV2 Anchor primer.

<400> 42
accaaagctt tggttttcag a 21

<210> 43
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> SPV3 Anchor primer.

<400> 43
tctgaaaacg tttgagtaga g 21

<210> 44
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> PVEcoRI primer.

<400> 44
tacatgaatt cgctcagtca ttatctttta ac 32

<210> 45
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Sigfor Bg1II primer.

<400> 45
agatctatgg cttcctccaa c 21

<210> 46
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Sigrev primer.

<400> 46
aaagataatg actgagcggc tgagtttgcg tg 32

<210> 47
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> SpM1forw primer.

<400> 47
cacgcaaact cagccgctca gtcattatct tt 32

<210> 48
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> APXhoI primer.

<400> 48
ctcgaggacc acgcgtatcg atgtcga 27

<210> 49
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Beta-subunit of the mannose lectin of Gowda et al.

<400> 49

Ala Gln Ser Leu Ser Phe Ser Ser Phe Thr Lys Phe Asp Pro Asn Gln
1 5 10 15

Glu Asp Leu Ile Phe Gln Gly Thr Ala Thr Ser Lys Leu Asp Ser Ala
20 25 30

Gly Asn Pro Val Ser Ser Ser Ala Gly Arg Val Leu Tyr Ser Ala Pro
35 40 45

Leu Arg Leu Trp Glu Asp Ser Ala Val Leu Thr Ser Phe Asp Pro Thr
50 55 60

Ile Tyr Ile Phe Thr Asn Tyr Thr Ser Arg Ile Ala Asp Gly Leu Ala
65 70 75 80

Phe Ile Ala Pro Pro Asp Ser Val Ile Ser Tyr His Gly Gly Phe Leu
85 90 95

Gly Leu Phe Pro Asn Ala Ala Glu Ser Gly
100 105

<210> 50
<211> 123
<212> PRT

<213> Artificial Sequence

<220>
<223> Beta-subunit of D1-FRIL.

<400> 50

Ala Gln Ser Leu Ser Phe Ser Phe Thr Lys Phe Asp Pro Asn Gln Glu
1 5 10 15

Asp Leu Ile Phe Gln Gly His Ala Thr Ser Thr Asn Asn Val Leu Gln
20 25 30

Val Thr Lys Leu Asp Ser Ala Gly Asn Pro Val Ser Ser Ser Ala Gly
35 40 45

Arg Val Leu Tyr Ser Ala Pro Leu Arg Leu Trp Glu Asp Ser Ala Val
50 55 60

Leu Thr Ser Phe Asp Thr Ile Ile Asn Phe Glu Ile Ser Thr Pro Tyr
65 70 75 80

Thr Ser Arg Ile Ala Asp Gly Leu Ala Phe Phe Ile Ala Pro Pro Asp
85 90 95

Ser Val Ile Ser Tyr His Gly Gly Phe Leu Gly Leu Phe Pro Asn Ala
100 105 110

Asn Thr Leu Asn Asn Ser Ser Thr Ser Glu Asn
115 120

<210> 51
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Alpha-subunit of the mannose lectin of Gowda et al.

<400> 51

Ile Ala Glu Ser Asn Val Val Ala Val Glu Phe Asp Thr Asp Tyr Leu
1 5 10 15

Asn Pro Asp Tyr Gly Asp Pro Asn Tyr Ile His Ile Gly Ile Asp Val
20 25 30

Asn Ser Ile Arg Ser Lys Val Thr Ala Ser Trp Asp Trp Gln Asn Gly
35 40 45

Lys Ile Ala Thr Ala His Ile Ser Tyr Asn Ser Val Ser Lys Arg Leu
50 55 60

Ser Val Thr Thr Tyr Tyr Pro Gly Arg Gly Lys Pro Ala Thr Ser Tyr
65 70 75 80

Asp Ile Glu Leu His Thr Val Leu Pro Glu Trp Val Arg Val Gly Leu
85 90 95

Ser Ala Ser Thr Gly Gln Asn Ile Glu Arg Asn Thr Val His Ser Trp
100 105 110

Ser Phe Thr Ser Ser Leu Trp Thr Asn Val Ala Lys Val Gly Val Ala
115 120 125

Ser Ile Ser Gly
130

<210> 52
<211> 147
<212> PRT
<213> Artificial Sequence

<220>
<223> Alpha-subunit of D1-FRIL.

<400> 52

Gln Thr Thr Thr Lys Ala Ala Ser Ser Asn Val Val Ala Val Glu Phe
1 5 10 15

Asp Thr Tyr Leu Asn Pro Asp Tyr Gly Asp Pro Asn Tyr Ile His Ile
20 25 30

Gly Ile Asp Val Asn Ser Ile Arg Ser Lys Val Thr Ala Lys Trp Asp
35 40 45

Trp Gln Asn Gly Lys Ile Ala Thr Ala His Ile Ser Tyr Asn Ser Val
50 55 60

Ser Lys Arg Leu Ser Val Thr Ser Tyr Tyr Ala Gly Ser Lys Pro Ala
65 70 75 80

Thr Leu Ser Tyr Asp Ile Glu Leu His Thr Val Leu Pro Glu Trp Val
85 90 95

Arg Val Gly Leu Ser Ala Ser Thr Gly Gln Asp Lys Glu Arg Asn Thr
100 105 110

Val His Ser Trp Ser Phe Thr Ser Ser Leu Trp Thr Asn Val Ala Lys
115 120 125

Lys Glu Asn Glu Asn Lys Tyr Ile Thr Arg Gly Val Leu Tyr Met Cys
130 135 140

Ile Asn Asp
145

<210> 53
<211> 64
<212> DNA

<213> Artificial Sequence

<220>
<223> Recombinant expression vector.

<400> 53
ctggttccgc gtggatcccc ggaattcatg cccggttcga ctcgagcggc cgcatcgtga 60

ctga 64

<210> 54
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombinant expression vector.

<400> 54
ctggttccgc gtggatcccc ggaattcatg ctcgagcggc cgcatcgtga ctga 54

<210> 55
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> DLL.

<400> 55

Ala Gln Ser Leu Ser Phe Ser Phe Thr Lys Phe Asp Pro Asn Gln Glu
1 5 10 15

Asp Leu Ile Phe Gln Gly Thr Ala Thr Ser Lys Leu Asp Ser Ala Gly
20 25 30

Asn Pro Val Ser Ser Ser Ala Gly Arg Val Leu Tyr Ser Ala Pro Leu
35 40 45

Arg Leu Trp Glu Asp Ser Ala Val Leu Thr Ser Phe Asp Pro Thr Ile
50 55 60

Tyr Ile Phe Thr Asn Tyr Thr Ser Arg Ile Ala Asp Gly Leu Ala Phe
65 70 75 80

Ile Ala Pro Pro Asp Ser Val Ile Ser Tyr His Gly Gly Phe Leu Gly
85 90 95

Leu Phe Pro Asn Ala Ala Glu Ser Gly Ile Ala Glu Ser Asn Val Val
100 105 110

Ala Val Glu Phe Asp Thr Asp Tyr Leu Asn Pro Asp Tyr Gly Asp Pro
115 120 125

Asn Tyr Ile His Ile Gly Ile Asp Val Asn Ser Ile Arg Ser Lys Val
130 135 140

Thr Ala Ser Trp Asp Trp Gln Asn Gly Lys Ile Ala Thr Ala His Ile
145 150 155 160

Ser Tyr Asn Ser Val Ser Lys Arg Leu Ser Val Thr Thr Tyr Tyr Pro
165 170 175

Gly Arg Gly Lys Pro Ala Thr Ser Tyr Asp Leu Glu Leu His Thr Val
180 185 190

Leu Pro Glu Trp Val Arg Val Gly Leu Ser Ala Ser Thr Gly Gln Asn
195 200 205

Ile Glu Arg Asn Thr Val His Ser Trp Ser Phe Thr Ser Ser Leu Trp
210 215 220

Thr Asn Val Ala Lys Val Gly Val Ala Ser Ile Ser Gly
225 230 235

<210> 56
<211> 279
<212> PRT
<213> Artificial Sequence

<220>
<223> PvFRIL.

<400> 56

Ala Gln Ser Leu Ser Phe Asn Phe Thr Lys Phe Asp Leu Asp Gln Lys
1 5 10 15

Asp Leu Ile Phe Gln Gly Asp Ala Thr Ser Thr Asn Asn Val Leu Gln
20 25 30

Leu Thr Lys Leu Asp Ser Gly Gly Asn Pro Val Gly Ala Ser Val Gly
35 40 45

Arg Val Leu Phe Ser Ala Pro Phe His Leu Trp Glu Asn Ser Met Ala
50 55 60

Val Ser Ser Phe Glu Thr Asn Leu Thr Ile Gln Ile Ser Thr Pro His
65 70 75 80

Pro Tyr Tyr Ala Ala Asp Gly Phe Ala Phe Phe Leu Ala Pro His Asp
85 90 95

Thr Val Ile Pro Pro Asn Ser Trp Gly Lys Phe Leu Gly Leu Tyr Ser
100 105 110

Asn Val Phe Arg Asn Ser Pro Thr Ser Glu Asn Gln Ser Phe Gly Asp

115 120 125

Val Asn Thr Asp Ser Arg Val Val Ala Val Glu Phe Asp Thr Phe Pro
130 135 140

Asn Ala Asn Ile Asp Pro Asn Tyr Arg His Ile Gly Ile Asp Val Asn
145 150 155 160

Ser Ile Lys Ser Lys Glu Thr Ala Arg Trp Glu Trp Gln Asn Gly Lys
165 170 175

Thr Ala Thr Ala Arg Ile Ser Tyr Asn Ser Ala Ser Lys Lys Ser Thr
180 185 190

Val Thr Thr Phe Tyr Pro Gly Met Glu Val Val Ala Leu Ser His Asp
195 200 205

Val Asp Leu His Ala Glu Leu Pro Glu Trp Val Arg Val Gly Leu Ser
210 215 220

Ala Ser Thr Gly Glu Glu Lys Gln Lys Asn Thr Ile Ile Ser Trp Ser
225 230 235 240

Phe Thr Ser Ser Leu Lys Asn Asn Glu Val Lys Glu Pro Lys Glu Asp
245 250 255

Met Tyr Ile Ala Asn Val Val Arg Ser Tyr Thr Trp Ile Asn Asp Val
260 265 270

Leu Ser Tyr Ile Ser Asn Lys
275

<210> 57
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<223> PHA-E.

<400> 57

Ala Ser Gln Thr Ser Phe Ser Phe Gln Arg Phe Asn Glu Thr Asn Leu
1 5 10 15

Ile Leu Gln Arg Asp Ala Thr Val Ser Ser Lys Gly Gln Leu Arg Leu
20 25 30

Thr Asn Val Asn Asp Asn Gly Glu Pro Thr Leu Ser Ser Leu Gly Arg
35 40 45

Ala Phe Tyr Ser Ala Pro Ile Gln Ile Trp Asp Asn Thr Thr Gly Ala
50 55 60

Val Ala Ala Ser Pro Thr Ser Phe Thr Phe Asn Ile Asp Val Pro Asn
65 70 75 80

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Asn Ser Gly Pro Ala Asp Gly Leu Ala Phe Val Leu Leu Pro Val Gly
                85                  90                  95

Ser Gln Pro Lys Asp Lys Gly Gly Leu Leu Gly Leu Phe Asn Asn Tyr
            100                 105                 110

Lys Tyr Asp Ser Asn Ala His Thr Val Ala Val Glu Phe Asp Thr Leu
        115                 120                 125

Tyr Asn Val His Trp Asp Pro Lys Pro Arg His Ile Gly Ile Asp Val
    130                 135                 140

Asn Ser Ile Lys Ser Ile Lys Thr Thr Thr Trp Asp Phe Val Lys Gly
145                 150                 155                 160

Glu Asn Ala Glu Val Leu Ile Thr Tyr Asp Ser Ser Thr Lys Leu Leu
                165                 170                 175

Val Ala Ser Leu Val Tyr Pro Ser Leu Lys Thr Ser Phe Ile Val Ser
            180                 185                 190

Asp Thr Val Asp Leu Lys Ser Val Leu Pro Glu Trp Val Ile Val Gly
        195                 200                 205

Phe Thr Ala Thr Thr Gly Ile Thr Lys Gly Asn Val Glu Thr Asn Asp
    210                 215                 220

Ile Leu Ser Trp Ser Phe Ala Ser Lys Leu Ser Asp Gly Thr Thr Ser
225                 230                 235                 240

Glu Ala Leu Asn Leu Ala Asn Phe Ala Leu Asn Gln Ile Leu
                245                 250
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